AMENDMENTS TO THE CLAIMS

1. (currently amended) A method of determining at least one of the biochemical or and biophysical properties of a protein, said method comprising the steps of:

    a) providing a database comprising protein sequence information and at least one of: protein biochemical properties and/or protein biophysical properties,

    b) analyzing the database using a data-mining technique, c) correlating to correlate one or more of the following: protein sequence, biochemical properties, and or biophysical properties, and

    dc) analyzing the sequence of the protein using the correlations to determine its biochemical or biophysical properties.

2. (original) The method of claim 1, wherein the property being determined is a biophysical property.

3. (currently amended) The method of claim 2, wherein the biophysical property is thermal stability, solubility, isoelectric point, pH stability, crystalizability, conditions of crystallization, aggregation state, heat capacity (DC_p), resistance to chemical denaturation, resistance to proteolytic degradation, amide hydrogen exchange data, behavior on chromatographic matrices, electrophoretic mobility, and resistance to degradation during mass spectrometry, and results obtained from nuclear magnetic resonance, X-ray crystallography, circular dichroism, light scattering, atomic adsorption, fluorescence, fluorescence quenching, mass spectroscopy, infrared spectroscopy, electron microscopy and atomic-force microscopy.

4. (withdrawn)

5. (original) The method of claim 3, wherein the biophysical property is solubility.

Claims 6-37   (withdrawn)

38. (original) The method of claim 1, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and support vector machines.

39. (original) The method of claim 38, wherein the data-mining technique is decision-tree analysis.

40.   (original) The method of claim 38, wherein the data-mining technique is case-based reasoning.

41.   (original) The method of claim 38, wherein the data-mining technique is Bayesian classifier.

42.   (original) The method of claim 38, wherein the data-mining technique is simple linear discriminant analysis.

43.   (original) The method of claim 38, wherein the data-mining technique is support vector machines.

Claims 44-57 (withdrawn)

58.   (currently amended) A method of optimizing high-throughput protein expression, said method comprising ~~the steps of~~:

    a) providing a database comprising protein sequence information and at least one of: protein biochemical properties and/~~or~~ protein biophysical properties,

    b) analyzing the database using a data-mining technique,~~c) correlating~~ to correlate one or more of the following: protein sequence, biochemical properties, and ~~or~~ biophysical properties,

    ~~d~~c) analyzing the sequence of the protein using the correlations to determine ~~its~~ at least one of the biochemical ~~or~~ and the biophysical properties of the protein, and

    ~~e~~d) optimizing throughput of the protein expression based on said biochemical or biophysical properties by modifying at least one of: ~~the~~ experimental procedures and/~~or modifying~~ the protein sequence.

59.   (original) The method of claim 58, wherein the data-mining technique is selected from the group decision-tree analysis, case-based reasoning, Bayesian classifier, simple linear discriminant analysis, and

60.   (original) The method of claim 59, wherein the data-mining technique is decision-tree analysis.

61.   (original) The method of claim 59, wherein the data-mining technique is case-based reasoning.

62.   (original) The method of claim 59, wherein the data-mining technique is Bayesian classifier.

63.   (original) The method of claim 59, wherein the data-mining technique is simple linear discriminant analysis.

64.   (original) The method of claim 59, wherein the data-mining technique is support vector machines.

Claims 65-66 (withdrawn)

67.   (New) The method of claim 2, where the biophysical property is based on data obtained from nuclear magnetic resonance, X-ray crystallography, circular dichroism, light scattering, atomic adsorption, fluorescence, fluorescence quenching, mass spectroscopy, infrared spectroscopy, electron microscopy, and atomic force microscopy.

68.   (New) The method of claim 1, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a large number of proteins which have been examined under uniform conditions.

69.   (New) The method of claim 1, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a variety of proteins wherein each protein's biochemical properties and biophysical properties have been determined under a variety of experimental conditions.

70.   (New) The method of claim 58, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a large number of proteins which have been examined under uniform conditions.

71.   (New) The method of claim 58, wherein the database comprises protein sequence information and at least one of: protein biochemical properties and protein biophysical properties for a variety of proteins wherein each protein's biochemical properties and biophysical properties have been determined under a variety of experimental conditions.